

SEQUENCE LISTING

COPY

<110> Dixon, Richard A.
Xia, Yiji
Lamb, Christopher

<120> CONSTITUTIVE DISEASE RESISTANCE (CDR1)
GENE AND METHODS OF USE THEREOF

<130> SALK2820-1

<140> 09/353,332

<141> 1999-07-14

<150> 60/092,696

<151> 1998-07-14

<160> 3

<170> FastSEQ for Windows Version 4.0

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<211> 4839

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<221> CDS

<222> (1111)...(2421)

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1

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FOOTNOTES: 1001555-103001

COPY

Ala Lys Pro Lys Leu Gly Phe Thr Ala Asp Leu Ile His Arg Asp Ser
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 Pro Lys Ser Pro Phe Tyr Asn Pro Met Glu Thr Ser Ser Gln Arg Leu
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cga aac gcg atc cac cga tcc gtt aac cgt gtt ttc cat ttc act gaa 1326
 Arg Asn Ala Ile His Arg Ser Val Asn Arg Val Phe His Phe Thr Glu
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aag gat aac aca cca caa cca cag att gac ctc acc tca aat agc ggt 1374
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 75 80 85

gaa tat ctc atg aac gta tcc att gga aca cct cct ttc ccg atc atg 1422
 Glu Tyr Leu Met Asn Val Ser Ile Gly Thr Pro Pro Phe Pro Ile Met
 90 95 100

gcc atc gcc gac acc gga agt gat ctc ctc tgg acg cag tgc gca cca 1470
 Ala Ile Ala Asp Thr Gly Ser Asp Leu Leu Trp Thr Gln Cys Ala Pro
 105 110 115 120

tgc gat gat tgt tac act caa gtt gat cct ctc ttt gac cct aaa acg 1518
 Cys Asp Asp Cys Tyr Thr Gln Val Asp Pro Leu Phe Asp Pro Lys Thr
 125 130 135

tct tcc aca tac aaa gac gtt tct tgc tcc tca agt caa tgt act gcc 1566
 Ser Ser Thr Tyr Lys Asp Val Ser Cys Ser Ser Ser Gln Cys Thr Ala
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cta gaa aat caa gcc tct tgt tcc aca aat gac aac act tgt tct tac 1614
 Leu Glu Asn Gln Ala Ser Cys Ser Thr Asn Asp Asn Thr Cys Ser Tyr
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 Ser Leu Ser Tyr Gly Asp Asn Ser Tyr Thr Lys Gly Asn Ile Ala Val
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gat acc tta acg ctc ggc tcc agc gat acc cgc cct atg cag ctt aag 1710
 Asp Thr Leu Thr Leu Gly Ser Ser Asp Thr Arg Pro Met Gln Leu Lys
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 Asn Ile Ile Ile Gly Cys Gly His Asn Asn Ala Gly Thr Phe Asn Lys
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 Lys Gly Ser Gly Ile Val Gly Leu Gly Gly Gly Pro Val Ser Leu Ile
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 Lys Gln Leu Gly Asp Ser Ile Asp Gly Lys Phe Ser Tyr Cys Leu Val
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 Pro Leu Thr Ser Lys Lys Asp Gln Thr Ser Lys Ile Asn Phe Gly Thr
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T0016358-103001

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Val Gly Ser Lys Gln Ile Gln Tyr Ser Gly Ser Asp Ser Glu Ser Ser
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Glu Gly Asn Ile Ile Ile Asp Ser Gly Thr Thr Leu Thr Leu Leu Pro
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Thr Glu Phe Tyr Ser Glu Leu Glu Asp Ala Val Ala Ser Ser Ile Asp
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Ala Thr Gly Asp Leu Lys Val Pro Val Ile Thr Met His Phe Asp Gly
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Ala Asp Val Lys Leu Asp Ser Ser Asn Ala Phe Val Gln Val Ser Glu
380 385 390

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Asp Leu Val Cys Phe Ala Phe Arg Gly Ser Pro Ser Phe Ser Ile Tyr
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          50          55          60
Asn Arg Val Phe His Phe Thr Glu Lys Asp Asn Thr Pro Gln Pro Gln
65          70          75          80
Ile Asp Leu Thr Ser Asn Ser Gly Glu Tyr Leu Met Asn Val Ser Ile
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Gly Thr Pro Pro Phe Pro Ile Met Ala Ile Ala Asp Thr Gly Ser Asp
          100          105          110
Leu Leu Trp Thr Gln Cys Ala Pro Cys Asp Asp Cys Tyr Thr Gln Val
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Asp Pro Leu Phe Asp Pro Lys Thr Ser Ser Thr Tyr Lys Asp Val Ser
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Tyr Thr Lys Gly Asn Ile Ala Val Asp Thr Leu Thr Leu Gly Ser Ser
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Asp Thr Arg Pro Met Gln Leu Lys Asn Ile Ile Ile Gly Cys Gly His
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COPY

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 275 280 285
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 305 310 315 320
 Gly Thr Thr Leu Thr Leu Leu Pro Thr Glu Phe Tyr Ser Glu Leu Glu
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 production; segment of SEQ ID NO:2

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10015510001